

# Boshou Liao

## List of Publications by Year in descending order

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43  
papers

1,493  
citations

279798

23  
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345221

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43  
docs citations

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times ranked

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citing authors

#	ARTICLE	IF	CITATIONS
1	Construction of ddRADseq-Based High-Density Genetic Map and Identification of Quantitative Trait Loci for Trans-resveratrol Content in Peanut Seeds. <i>Frontiers in Plant Science</i> , 2021, 12, 644402.	3.6	14
2	Dissection of the Genetic Basis of Yield-Related Traits in the Chinese Peanut Mini-Core Collection Through Genome-Wide Association Studies. <i>Frontiers in Plant Science</i> , 2021, 12, 637284.	3.6	18
3	Key Regulators of Sucrose Metabolism Identified through Comprehensive Comparative Transcriptome Analysis in Peanuts. <i>International Journal of Molecular Sciences</i> , 2021, 22, 7266.	4.1	14
4	High-Density Genetic Linkage Map Construction Using Whole-Genome Resequencing for Mapping QTLs of Resistance to <i>Aspergillus flavus</i> Infection in Peanut. <i>Frontiers in Plant Science</i> , 2021, 12, 745408.	3.6	9
5	High-resolution mapping of a major and consensus quantitative trait locus for oil content to a ~0.8-Mb region on chromosome A08 in peanut ( <i>Arachis hypogaea</i> L.). <i>Theoretical and Applied Genetics</i> , 2020, 133, 37-49.	3.6	33
6	Genome-wide expression quantitative trait locus analysis in a recombinant inbred line population for trait dissection in peanut. <i>Plant Biotechnology Journal</i> , 2020, 18, 779-790.	8.3	14
7	Optimization of extraction of total trans-resveratrol from peanut seeds and its determination by HPLC. <i>Journal of Separation Science</i> , 2020, 43, 1024-1031.	2.5	17
8	Identification of Two Novel Peanut Genotypes Resistant to Aflatoxin Production and Their SNP Markers Associated with Resistance. <i>Toxins</i> , 2020, 12, 156.	3.4	15
9	Discovery of two novel and adjacent QTLs on chromosome B02 controlling resistance against bacterial wilt in peanut variety Zhonghua 6. <i>Theoretical and Applied Genetics</i> , 2020, 133, 1133-1148.	3.6	14
10	Transcriptome and metabolome reveal redirection of flavonoids in a white testa peanut mutant. <i>BMC Plant Biology</i> , 2020, 20, 161.	3.6	28
11	Four QTL clusters containing major and stable QTLs for saturated fatty acid contents in a dense genetic map of cultivated peanut ( <i>Arachis hypogaea</i> L.). <i>Molecular Breeding</i> , 2019, 39, 1.	2.1	17
12	Mitigating Aflatoxin Contamination in Groundnut through A Combination of Genetic Resistance and Post-Harvest Management Practices. <i>Toxins</i> , 2019, 11, 315.	3.4	73
13	Next-generation sequencing identified genomic region and diagnostic markers for resistance to bacterial wilt on chromosome B02 in peanut ( <i>Arachis hypogaea</i> L.). <i>Plant Biotechnology Journal</i> , 2019, 17, 2356-2369.	8.3	41
14	Identification of genomic regions and diagnostic markers for resistance to aflatoxin contamination in peanut ( <i>Arachis hypogaea</i> L.). <i>BMC Genetics</i> , 2019, 20, 32.	2.7	37
15	Discovery of genomic regions and candidate genes controlling shelling percentage using QTL-seq approach in cultivated peanut ( <i>Arachis hypogaea</i> L.). <i>Plant Biotechnology Journal</i> , 2019, 17, 1248-1260.	8.3	51
16	Genome-wide systematic characterization of bZIP transcription factors and their expression profiles during seed development and in response to salt stress in peanut. <i>BMC Genomics</i> , 2019, 20, 51.	2.8	42
17	Transcriptomic profiling reveals pigment regulation during peanut testa development. <i>Plant Physiology and Biochemistry</i> , 2018, 125, 116-125.	5.8	15
18	Chromosomes A07 and A05 associated with stable and major QTLs for pod weight and size in cultivated peanut ( <i>Arachis hypogaea</i> L.). <i>Theoretical and Applied Genetics</i> , 2018, 131, 267-282.	3.6	49

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19	A Major and Stable QTL for Bacterial Wilt Resistance on Chromosome B02 Identified Using a High-Density SNP-Based Genetic Linkage Map in Cultivated Peanut Yuanza 9102 Derived Population. <i>Frontiers in Genetics</i> , 2018, 9, 652.	2.3	27
20	Stable QTLs for Plant Height on Chromosome A09 Identified From Two Mapping Populations in Peanut ( <i>Arachis hypogaea</i> L.). <i>Frontiers in Plant Science</i> , 2018, 9, 684.	3.6	21
21	Development of a High-Density Genetic Map Based on Specific Length Amplified Fragment Sequencing and Its Application in Quantitative Trait Loci Analysis for Yield-Related Traits in Cultivated Peanut. <i>Frontiers in Plant Science</i> , 2018, 9, 827.	3.6	56
22	Dynamic transcriptome landscape of sesame ( <i>Sesamum indicum</i> L.) under progressive drought and after rewatering. <i>Genomics Data</i> , 2017, 11, 122-124.	1.3	24
23	Development of SSR markers and identification of major quantitative trait loci controlling shelling percentage in cultivated peanut ( <i>Arachis hypogaea</i> L.). <i>Theoretical and Applied Genetics</i> , 2017, 130, 1635-1648.	3.6	48
24	Transcriptomic, biochemical and physio-anatomical investigations shed more light on responses to drought stress in two contrasting sesame genotypes. <i>Scientific Reports</i> , 2017, 7, 8755.	3.3	62
25	Co-localization of major quantitative trait loci for pod size and weight to a 3.7ÂcM interval on chromosome A05 in cultivated peanut ( <i>Arachis hypogaea</i> L.). <i>BMC Genomics</i> , 2017, 18, 58.	2.8	54
26	Genome evolutionary dynamics followed by diversifying selection explains the complexity of the <i>Sesamum indicum</i> genome. <i>BMC Genomics</i> , 2017, 18, 257.	2.8	17
27	Mutant Transcriptome Sequencing Provides Insights into Pod Development in Peanut ( <i>Arachis</i> ) Tj ETQq1 1 0.784314 rgBT /Overlock 10 Tf 50 3	3.6	23
28	Genetic Variation and Association Mapping of Seed-Related Traits in Cultivated Peanut ( <i>Arachis</i> ) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 3 2105.	3.6	27
29	Evolutionary history and functional divergence of the cytochrome P450 gene superfamily between <i>Arabidopsis thaliana</i> and <i>Brassica</i> species uncover effects of whole genome and tandem duplications. <i>BMC Genomics</i> , 2017, 18, 733.	2.8	37
30	PMDBase: a database for studying microsatellite DNA and marker development in plants. <i>Nucleic Acids Research</i> , 2017, 45, D1046-D1053.	14.5	46
31	Comprehensive Screening of Some West and Central African Sesame Genotypes for Drought Resistance Probing by Agromorphological, Physiological, Biochemical and Seed Quality Traits. <i>Agronomy</i> , 2017, 7, 83.	3.0	29
32	Analysis of Genetic Diversity and Population Structure of Sesame Accessions from Africa and Asia as Major Centers of Its Cultivation. <i>Genes</i> , 2016, 7, 14.	2.4	51
33	Characterization and Transferable Utility of Microsatellite Markers in the Wild and Cultivated <i>Arachis</i> Species. <i>PLoS ONE</i> , 2016, 11, e0156633.	2.5	21
34	Transcriptome Analysis of a New Peanut Seed Coat Mutant for the Physiological Regulatory Mechanism Involved in Seed Coat Cracking and Pigmentation. <i>Frontiers in Plant Science</i> , 2016, 7, 1491.	3.6	39
35	Development and deployment of a high-density linkage map identified quantitative trait loci for plant height in peanut ( <i>Arachis hypogaea</i> L.). <i>Scientific Reports</i> , 2016, 6, 39478.	3.3	76
36	Genomic survey sequencing for development and validation of single-locus SSR markers in peanut ( <i>Arachis hypogaea</i> L.). <i>BMC Genomics</i> , 2016, 17, 420.	2.8	33

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37	Quantitative trait locus analysis for pod- and kernel-related traits in the cultivated peanut ( <i>Arachis</i> ) Tj ETQq1 1 0.784314 rgBT/Overlook	2.7	70
38	Quantitative Trait Locus Analysis of Late Leaf Spot Resistance and Plant-Type-Related Traits in Cultivated Peanut ( <i>Arachis hypogaea</i> L.) under Multi-Environments. PLoS ONE, 2016, 11, e0166873.	2.5	51
39	Genome-wide analysis of the basic leucine zipper (bZIP) transcription factor gene family in six legume genomes. BMC Genomics, 2015, 16, 1053.	2.8	93
40	PTGBase: an integrated database to study tandem duplicated genes in plants. Database: the Journal of Biological Databases and Curation, 2015, 2015, .	3.0	46
41	The Peanut ( <i>Arachis hypogaea</i> L.) Gene AhLPAT2 Increases the Lipid Content of Transgenic Arabidopsis Seeds. PLoS ONE, 2015, 10, e0136170.	2.5	15
42	Phenotypic evaluation of the Chinese mini-mini core collection of peanut ( <i>Arachis hypogaea</i> L.) and assessment for resistance to bacterial wilt disease caused by <i>Ralstonia solanacearum</i> . Plant Genetic Resources: Characterisation and Utilisation, 2013, 11, 77-83.	0.8	11
43	Genomic affinities of <i>Arachis</i> genus and interspecific hybrids were revealed by SRAP markers. Genetic Resources and Crop Evolution, 2010, 57, 903-913.	1.6	15